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Display Show Range: from to Features: ☐ SNP ☒ CDD ☒ MGC ☒ HPRD ☒ STS ☒ tRNA ☐ 1: [AAC83379](#). Reports structural polypr...[gi:3978527][BLink](#), [Links](#)Features Sequence

LOCUS AAC83379 1245 aa linear VRL 11-MAY-2000

DEFINITION structural polyprotein [Sindbis virus].

ACCESSION AAC83379

VERSION AAC83379.1 GI:3978527

DBSOURCE locus AF103728 accession [AF103728.1](#)

KEYWORDS .

SOURCE Sindbis virus

ORGANISM Sindbis virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; WEEV complex.

REFERENCE 1 (residues 1 to 1245)

AUTHORS Liang,G.D., Li,L., Zhou,G.L., Fu,S.H., Li,Q.P., Li,F.S., He,H.H., Jin,Q., He,Y., Chen,B.Q. and Hou,Y.D.

TITLE Isolation and complete nucleotide sequence of a Chinese Sindbis-like virus

JOURNAL J. Gen. Virol. 81 (Pt 5), 1347-1351 (2000)

PUBMED [10769078](#)

REFERENCE 2 (residues 1 to 1245)

AUTHORS Li,L., Liang,G.D., Zhou,G.L., Fu,S.H., Jin,Q. and Hou,Y.D.

TITLE Direct Submission

JOURNAL Submitted (01-NOV-1998) State Key Laboratory for Molecular Virology and Genetic Engineering, Institute of Virology, CAPM, Ying Xin Jie 100#, Xuan Wu Qu, Beijing 100052, China

COMMENT Method: conceptual translation supplied by author.

FEATURES

Location/Qualifiers

source 1..1245
 /organism="Sindbis virus"
 /strain="XJ-160"
 /db_xref="taxon:11034"
 /lab_host="BHK-21"
 /country="China"

Protein 1..1245
 /product="structural polyprotein"

mat_peptide 1..264
 /product="capsid protein"

mat_peptide 265..328
 /product="E3"

mat_peptide 329..751
 /product="E2"

mat_peptide 752..806
 /product="6K"

mat_peptide 807..1245
 /product="E1"

CDS 1..1245
 /coded_by="AF103728.1:7569..11306"

ORIGIN

 751
 329

 422

1 mnrgffnmlg rrpfpaptsm wrprrrrrqaa pmparnglas qiqqlttavs alviggaarp
61 qqprprpppr qkkqppkqlp kpkkpktqdk kkrqpakpqp gkrqrmalkl eadrlfdvkn
121 engdvighal amegkvmkpl hvkgtidhpv lsklkftkss aydmefaqpl vnmrseafy
181 tsehpegfyn whhgavqysg grftiprgvg grgdsgrpim dnagrvaiv lggadegtrt
241 alsvvtwnsk gktiktspeg teewsaaplv tamcllgnvs fpcnrpptyc trepsraldi
301 leenvnhedy dtlldailnc dfsgnrnkrsv tgdftltspy lgtcpsychht epcfspikie
361 qvwdepddtt iriqtsaqfg ydqsgatsvn kyrymsfdqd htvkeggmdd ikistsgpcr
421 rlghkgyfll akcppgdsvt vsivsssstt sctlarkikp kfvgrerydl ppvygkhihc
481 mydrlkets agyitmhrpg phaytsylee asgkiyakpp sgknityeck cgdyktgtvk
541 trteitgcta ikqcvayksd qtkwvfnspd lirhadhaaq gklhlpfrlv pssckvpvah
601 apsvvhgfkx islqldtdhl tllttrrlga npeptsewii gktvrnfsvg rdgleytwgn
661 hdpvrvyage sapgdphgwp heiiqhyyhr hpaytiltvv saavavligl tvaalctcka
721 rrecltpyal apnavvptsi allccirsan aefsetmsy lwsnsqpffw aqlciplaav
781 vilvrccscclpflvvagvy lgkvdayeha ttipnvpkip ykalversgy aplnleitvv
841 ssqvlpstng eyitckfttv vpspkvkccg slecqaaha dynckvfggv ypfmwggaqc
901 fcdsentoms eayvklisadcl vtdyaqavnv htaamkvglr ivygnntsyl dvyvngvtpg
961 tskdlkviag pvsssftpfh hkvvviyrglv ynydfpeyga mkpgvfgdiq atsltsrdli
1021 astdirllkp svknvhvpyt qaasgfemwk nnsgrplqet apfgckiavn plravdcsyg
1081 nipisidipn aafirisdap lvstvkcevs gctysadfgg matlqyvsvr egqcpvhshs
1141 statlqestv hvlekgavtv hfstaspqan fiislcgkkt tcnaeckppa dhivstphki
1201 dqefqtaisk tswswllalf ggasslliig lmiftcsmlt tstrr

nipcr

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☐ 1: [AAA96973](#). Reports structural polypr...[gi:334113]

BLink, Links

Features Sequence

LOCUS AAA96973 1245 aa linear VRL 13-FEB-2003
 DEFINITION structural polyprotein [Ockelbo virus].
 ACCESSION AAA96973
 VERSION AAA96973.1 GI:334113
 DBSOURCE locus SINOCK82 accession [M69205.1](#)
 KEYWORDS .
 SOURCE Ockelbo virus
 ORGANISM Ockelbo virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 Alphavirus; WEEV complex.
 REFERENCE 1 (residues 1 to 1245)
 AUTHORS Shirako,Y., Niklasson,B., Dalrymple,J.M., Strauss,E.G. and
 Strauss,J.H.
 TITLE Structure of the Ockelbo virus genome and its relationship to other
 Sindbis viruses
 JOURNAL Virology 182 (2), 753-764 (1991)
 PUBMED [1673813](#)

FEATURES Location/Qualifiers
 source 1..1245
 /organism="Ockelbo virus"
 /strain="Edsbyn 82-5"
 /isolate="Ockelbo 82"
 /db_xref="taxon:31699"
Protein 1..1245
 /product="structural polyprotein"
mat_peptide 1..264
 /product="C"
mat_peptide 265..328
 /product="E3"
mat_peptide 329..751
 /product="E2"
mat_peptide 752..806
 /product="6K"
mat_peptide 807..1245
 /product="E1"
CDS 1..1245
 /coded_by="M69205.1:7653..11390"

ORIGIN

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121 edgdvighal amegkvmpkl hvkgtidhpv lsklkftkss aydmefaqlp vnmrseafy
181 tsehpegfyn whhgavqysg grftiprgvg grgdsgrpm dnsgrvvaiv lggadegtrt
241 alsvvtwnsk gktikttepeg teewsaaplv tamcllgns fpcnrpptyc trepsraldi
301 leenvnheay dtllnailrc gssgrskrsv tddftltspy lgtcsychht epcfspikie
361 qvwdeaddnt iriqtsaqfg ydksgaastn kyrymsfeqd htvkegtmdd ikistsgpcr
421 rlsykgyfll akcpvgdsvt vsiassnsat sctmarkikp kfvgrekydl ppvhgkkip

```

751
329-
423

kipc-e

481 t~~h~~vydrlkett agyitmhrpg phaytsylee ssgkvyakpp sgknityeck cgdyktgtvt
541 trteitgcta ikqcvayksd qtkwvfnsdp lirhadhtaq gklhlpfkli pstcmvpvah
601 apnvihgfkx islqltdthl tllttrrlga npepttewii gktvrnftvd rdgleyiwgn
661 hepvrvyage sapgdphgwp heivqhyhrr hpvytilava saavammigv tvaalcacka
721 rrecltpyal apnaviptsl allccvrsan aetftetmsy fwsnsqpffw vqlciplaav
781 ivlmrccsccl pflvvagay lakvdayeha ttvpnvpgip ykalveragy aplnleitvm
841 ssevlpstnq eyitckfttv vpspkvkccg slecqpaaah dytckvfggv ypfmwggagc
901 fcdsensqms eayvelsadc atdhaqaikv htaamkvglr ivygnntsfl dvyvngvtpg
961 tskdlkviag piasasftpfd hkvvihrglv ynydfpeyga mkpgvfgdiq atsltskdli
1021 astdirllkp saknvhvpyt qaasgfemwk nnsgrplqet apfgckiavn plravdcsyg
1081 nipisidipn aafirtsdap lvstvkcdvs ectysadfgg matlqyvsvr egqcpvhshs
1141 statlqestv hvlekgavtv hfstaspqan fivslcgkkt tcnaeckppa dhivstphkn
1201 dgefqaaisk tswswlfalf ggasslliig ltifacsmml tstrr

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☐ 1: [AAO33347](#). Reports structural polypr...[gi:28193973]

BLink, Links

Features Sequence

LOCUS AAO33347 ✓ 1239 aa linear VRL 02-FEB-2003
 DEFINITION structural polyprotein precursor [Barmah Forest virus].
 ACCESSION AAO33347
 VERSION AAO33347.1 GI:28193973
 DBSOURCE accession [AF339488.1](#)
 KEYWORDS .
 SOURCE Barmah Forest virus
 ORGANISM Barmah Forest virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.
 REFERENCE 1 (residues 1 to 1239)
 AUTHORS Kinney,R.M. and Pfeffer,M.
 TITLE Nucleotide sequence analyses of the 26S mRNAs of viruses of the genus Alphavirus
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1239)
 AUTHORS Kinney,R.M. and Pfeffer,M.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2001) Arbovirus Diseases Branch, Centers for Disease Control and Prevention, P.O. Box 2087, Fort Collins, CO 80522, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..1239
 /organism="Barmah Forest virus"
 /virion
 /strain="BH 2193"
 /db_xref="taxon:11020"
 /country="Australia"
 /note="isolated in 1974; virus passage P7/SM2/BHK21-1"
 Protein 1..1239
 /product="structural polyprotein precursor"
 mat_peptide 1..253
 /product="capsid protein"
 mat_peptide 254..321
 /product="E3 protein"
 mat_peptide 322..742
 /product="E2 envelope glycoprotein"
 mat_peptide 743..800
 /product="6K protein"
 mat_peptide 801..1239
 /product="E1 envelope glycoprotein"
 CDS 1..1239
 /coded_by="AF339488.1:603..4322"

ORIGIN

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742
 222
 520

61 raqkkpkktpp pppkpkktqkp kkptqkkkssk pgkrmrncmk iendcifpvm ldgkvngyac
121 lvgdkvmpka hvkgtidnpe lakltfkkss kydlecaqvp vcmksdaskf thekpeghyn
181 whhgavqfsn grftiptgsg kpgdsgrpif dntgkvvaiv lgganegart alsvvtwnkd
241 mvtritpees vewsaaalni talcvlqnls fpcdappcap ccyekdpagt lrlldshyyh
301 pkyyelldst' mhcpqgrrpk' rs' vahfeayk atrpyigwca dcglagscps pvsiehvwsd
361 addgvlkiqv smqigiaksn tinhakirym gangvqeaer stlsvsttap cdilatmghf
421 ilarcrpgsq yevslstdpk llcrtpfshk prfigneksp aptghktrip cktyshtdl
481 treeitmhvp pdvpiqglvs ntgksysldp ktktikykct cgetvkegta tnkitlfncl
541 tapkcityav dntvwqynsq yvprsevev kgkihvpfpl tdstcavsva pepqvtlyrlg
601 evefhfhpmyp tlfslsirlg kdpshsqewi dtpmsktiqv gaegveyvwg nnpvrlwaq
661 kssssahgn pisivshyyd lypywtitvl aslgllivis sgfscflcsv artkcltpyq
721 lapgaqlptf iallccaksa radlddfsy lwtnnqamfw lqlaspvaaf lclsyccrnl
781 accmkiflgi sglcviatqa yehsttmpnq vgipfkalie rpgyaalpls lvvikselvp
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901 scmsevyvtr gesceadhai ayqvhtask aqvmisigel ngtvdfvng dspariqqsk
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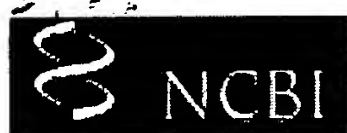

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 ☒ tRNA
 ☒ RefSeq

☐ 1: [AAO33325](#). Reports structural polypr...[gi:28193940]

[BLink](#), [Links](#)

Features Sequence

LOCUS AAO33325 1245 aa linear VRL 02-FEB-2003
 DEFINITION structural polyprotein precursor [Babanki virus].
 ACCESSION AAO33325
 VERSION AAO33325.1 GI:28193940
 DBSOURCE accession [AF339477.1](#)
 KEYWORDS .
 SOURCE Babanki virus
 ORGANISM Babanki virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; WEEV complex.
 REFERENCE 1 (residues 1 to 1245)
 AUTHORS Kinney,R.M. and Pfeffer,M.
 TITLE Nucleotide sequence analyses of the 26S mRNAs of viruses of the genus Alphavirus
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 1245)
 AUTHORS Kinney,R.M. and Pfeffer,M.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2001) Arbovirus Diseases Branch, Centers for Disease Control and Prevention, P.O. Box 2087, Fort Collins, CO 80522, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..1245
 /organism="Babanki virus"
 /virion
 /strain="DakAry 251"
 /db_xref="taxon:48540"
 /country="Cameroon"
 /note="isolated in 1969; virus passage P?/SM2/BHK21-1"
 Protein 1..1245
 /product="structural polyprotein precursor"
 mat_peptide 1..264
 /product="capsid protein"
 mat_peptide 265..328
 /product="E3 protein"
 mat_peptide 329..751
 /product="E2 envelope glycoprotein"
 mat_peptide 752..806
 /product="6K protein"
 mat_peptide 807..1245
 /product="E1 envelope glycoprotein"
 CDS 1..1245
 /coded_by="AF339477.1:619..4356"

ORIGIN

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121 edgdvighal amegkvmkpl hvkgtidhpv lsklkftkss aydmefaqlp vnmrseafy
181 tsehpegfyn whhgavqysg grftiprgvg grgdsgrpm dnsgrvvaiv lggadegtrt
241 alsvtwnsk gktiktpeg teewsaaplv tamcllgnvs fpcnrppty trepsraldi
301 leenvnheay dtllnailrc gssgrskrs* tddftltspy lgtcsychht epcfspikie
361 qvwdeaddnt iriqtsaqfg ydqsgaastn kyrymsleqd htvkegtmdd ikistsgpcr
421 rlsykgyfll akcppgdsvt vsiassnsat sctmarkikp kfvgrekydl ppvhgkkipc
481 tvydrlkett agyitmhrpg phaytsylee ssgkvyakpp sgknityecq cgdyktgtvt
541 trteitgcta ikqcvayksd qtkwvfnspd lirhadhtaq gklhlpfkli pstcmvpvah
601 apnvihgfkhl islqldtdhl tllttrrlga npepttewii gktvrnftvd rdgleyiwn
661 hepvrvyaqe sapgdphgwp heivqhyhr hpvytilava savvammigv tvaalcacka
721 rrecltpyal apnaviptsl allccvrsan aetftetmsy lwsnsqpffw vqlciplaav
781 ivlmrccscc lpflvvagay lakvdayeha ttvpnpqip ykalveragy aplnleitvm
841 ssevlpstnq eyitckfttv vpspkvkccg slecqpaaah dytckvfggv ypfmwggaqc
901 fcdsensqms eayvelsadc atdhaqavkv htaamkvglr ivygnttsfl dvyvngvtpg
961 tskdlkviag pisasftpfd hkvvihrglv ynydfpeyga mkpgafgdiq atsltskdli
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